

# Consensus Sequence

Symbol comparison table: blosum62.cmp CompCheck: 6430

Name: <u>hTRADEalpha_1</u>	Len: 423	Check: 4050	Weight: 1.00
Name: <u>hTRAIN_1</u>	Len: 423	Check: 4128	Weight: 1.00
Name: <u>hTRADEbeta_1</u>	Len: 423	Check: 7937	Weight: 1.00
Name: <u>hApo420pep</u>	Len: 423	Check: 8173	Weight: 1.00

```
//
      1
hTRADEalpha_ MALKVLLLEQE KTFFTLLVLL GYLSCKVTC E SGDCRQQEFR DRSQNCVPCN
hTRAIN_1      MALKVLLLEQE KTFFTLLVLL GYLSCKVTC E SGDCRQQEFR DRSQNCVPCN
hTRADEbeta_1  MALKVLLLEQE KTFFTLLVLL GYLSCKVTC E SGDCRQQEFR DRSQNCVPCN
hApo420pep    MALKVLLLEQE KTFFTLLVLL GYLSCKVTC E SGDCRQQEFR DRSQNCVPCN
Consensus     MALKVLLLEQE KTFFTLLVLL GYLSCKVTC E SGDCRQQEFR DRSQNCVPCN

      51
hTRADEalpha_ QCQPGMELSK ECQFGYGEDA QCVTCRLHRF KEDWGFQKCK PCLDCAVVNR
hTRAIN_1      QCQPGMELSK ECQFGYGEDA QCVTCRLHRF KEDWGFQKCK PCLDCAVVNR
hTRADEbeta_1  QCQPGMELSK ECQFGYGEDA QCVTCRLHRF KEDWGFQKCK PCLDCAVVNR
hApo420pep    QCQPGMELSK ECQFGYGEDA QCVTCRLHRF KEDWGFQKCK PCLDCAVVNR
Consensus     QCQPGMELSK ECQFGYGEDA QCVTCRLHRF KEDWGFQKCK PCLDCAVVNR

      101
hTRADEalpha_ FQKANC SATS DAICQDCLPG FYRKTCLVGF QDMECVPCGD PPPPYEPHCA
hTRAIN_1      FQKANC SATS DAICQDCLPG FYRKTCLVGF QDMECVPCGD PPPPYEPHCA
hTRADEbeta_1  FQKANC SATS DAICQDCLPG FYRKTCLVGF QDMECVPCGD PPPPYEPHCA
hApo420pep    FQKANC SATS DAICQDCLPG FYRKTCLVGF QDMECVPCGD PPPPYEPHCA
Consensus     FQKANC SATS DAICQDCLPG FYRKTCLVGF QDMECVPCGD PPPPYEPHCA

      151
hTRADEalpha_ SKVNLVKIAS TASSPRDTAL AAVICSALAT VLLALLILCV IYCKRQFM EK
hTRAIN_1      SKVNLVKIAS TASSPRDTAL AAVICSALAT VLLALLILCV IYCKRQFM EK
hTRADEbeta_1  SKVNLVKIAS TASSPRDTAL AAVICSALAT VLLALLILCV IYCKRQFM EK
hApo420pep    SKVNLVKIAS TASSPRDTAL AAVICSALAT VLLALLILCV IYCKRQFM EK
Consensus     SKVNLVKIAS TASSPRDTAL AAVICSALAT VLLALLILCV IYCKRQFM EK

      201
hTRADEalpha_ KPSWSLRSQD IQYNGSELSC FDRPQLHEYA HRACCQCR RD SVQTCGPFVRL
hTRAIN_1      KPSWSLRSQD IQYNGSELSC FDRPQLHEYA HRACCQCR RD SVQTCGPFVRL
hTRADEbeta_1  KPSWSLRSQD IQYNGSELSC LDRPQLHEYA HRACCQCR RD SVQTCGPFVRL
hApo420pep    KPSWSLRSQD IQYNETELSC FDRPQLHEYA HRACCQCR RD SVQTCGPFVRL
Consensus     KPSWSLRSQD IQYNGSELSC FDRPQLHEYA HRACCQCR RD SVQTCGPFVRL

      251
hTRADEalpha_ LPSMCCEEAC SPNPATLQCG VHS AASLOAR NAGPAGEMVP TFFGSLTQSI
hTRAIN_1      LPSMCCEEAC SPNPATLQCG VHS AASLOAR NAGPAGEMVP TFFGSLTQSI
hTRADEbeta_1  LPSMCCEEAC SPNPATLQCG VHS AASLOAR NAGPAGEMVP TFFGSLTQSI
hApo420pep    LPSMCCEEAC SPNPATLQCG VHS AASLOAR NAGPAGEMVP TFFGSLTQSI
Consensus     LPSMCCEEAC SPNPATLQCG VHS AASLOAR NAGPAGEMVP TFFGSLTQSI
```

Figure 1

301 350

hTRADEalpha_	CQ	MONPMGGONI	SFCDSYPFLT	GEDT	LESSTSLDSN
hTRAIN_1	CQ	MONPMGGONI	SFCDSYPFLT	GEDT	LESSTSLDSN
hTRADEbeta_1	CGEFSDAWPL	MONPMGGONI	SFCDSYPFLT	GEDINSLAPE	LESSTSLDSN
hApo420pep	CGEFSDAWPL	MONPMGGONI	SFCDSYPFLT	GEDINSLAPE	LESSTSLDSN
Consensus	CGEFSDAWPL	MONPMGGONI	SFCDSYPFLT	GEDINSLAPE	LESSTSLDSN

351 400

hTRADEalpha_	SSQDLVGQAV	PVQSHSENFT	AATDLSRYNN	TLVESASTQD	ALTMRSQLDQ
hTRAIN_1	SSQDLVGQAV	PVQSHSENFT	AATDLSRYNN	TLVESASTQD	ALTMRSQLDQ
hTRADEbeta_1	SSQDLVGQAV	PVQSHSENFT	AATDLSRYNN	TLVESASTQD	ALTMRSQLDQ
hApo420pep	SSQDLVGQAV	PVQSHSENFT	AATDLSRYNN	TLVESASTQD	ALTMRSQLDQ
Consensus	SSQDLVGQAV	PVQSHSENFT	AATDLSRYNN	TLVESASTQD	ALTMRSQLDQ

401 423

hTRADEalpha_	ESQAIHPAT	QTSLQEA---	---
hTRAIN_1	ESQAVIHPAT	QTSLQEA---	---
hTRADEbeta_1	ESQAIHPAT	QTSLQVRQRL	GSL
hApo420pep	ESQAVIHPAT	QTSLQVRQRL	GSL
Consensus	ESQA-IHPAT	QTSLQ--QRL	GSL

097653E 020904  
T06020 25599750

Figure 1

TRADE- $\alpha$   
TRADE- $\beta$

ESGAIHPATQTSLQEA  
ESGAIHPATQTSLQVRQLGSL

401 416 423

**Figure 2**

## CRD1

NGF75  
OX40  
CD40  
TRADE

QFTGLYF.H	SGA.C	..CK.C	MLGECVAGSC	..G.AWQTYCE
QADTYF..S	NDK.C	..CH.C	RPCGCVVSC	..SASQNTYCR
QREKQYL.I	NSCC	..CS.C	QPGQQLVSC	..TITTTZTCL
CRQGEPRDR	SGCVVSC	..CH.C	GPCVLELSC	GPCYQEDACV

## CRD2

NGF75  
OX40  
CD40  
TRADE

KOLDSTVTS	DVSEATKOK	SGTACVGLAS	MSAP...	QVE	ADDAVC
PC..GPGFY	NDVSSSTOK	SGTAC.HLRB	GSERKQLOTA	TQDTTC	
SGCES.IPL	DVSEATKOK	QKESODPHLG	LVVQORGTSE	T.DTTC	
TORLER.VK	KDNGVOK.OK	KOLDVAVH	..KPOKARSA	TSQATC	

Figure 3

SEQ ID NO:2 Human TRADE $\alpha$   
 SEQ ID NO:6 Mouse Trade

CRD1  
 MAIKVILEQEKTEFTLLVLGYISKTTHESDGRQQLFRFSSQAMPON  
 MAIKVILPLHRTVLAAAILFLHAAKVSCTEIRKQCEKKEKTHHNLK

SEQ ID NO:2 Human TRADE $\alpha$   
 SEQ ID NO:6 Mouse Trade

CRD2  
 ECGPGMMLSKEDGQYGEDAQVTCRIIRFKHEDCFCKKPKCLDCAVDFP  
 EIRPGMMLSKEDGQYGEDAQVTCRIIRFKHEDCFCKKPKCLDCAVDFP

SEQ ID NO:2 Human TRADE $\alpha$   
 SEQ ID NO:6 Mouse Trade

↓ 143 ?  
 FOKANGSATSDAIGGLCLGFEYRFTKINGQFQMEQVEGQDFPPFYEPICA  
 FOKANGSHHIDAVQADCLGFEYRFTKINGQFQMEQVEGQDFPPFYEPICAT

SEQ ID NO:2 Human TRADE $\alpha$   
 SEQ ID NO:6 Mouse Trade

167 TM 192  
 SKYNIYKIASTRSSPRDTAAAVTCSALATVLLALLTLQVITYCKRQFMEN  
 SKYNIYKISSTRSSPRDTAAAVTCSALATVLLALLTLQVITYCKRQFMEN

SEQ ID NO:2 Human TRADE $\alpha$   
 SEQ ID NO:6 Mouse Trade

KRWSTLRSDQYHGELESCFTTRPQIHEYAHRACQCRKDEVQTCQFVRI  
 KRWSTLRSDQYHGELESCFTTRPQIRHCAHRACQYHRDSAPMYLPHVI

SEQ ID NO:2 Human TRADE $\alpha$   
 SEQ ID NO:6 Mouse Trade

LEDMCELRACPNPFTLQGVHAAASLCANNAGPACEMVETFEGLTQST  
 IESLKEHARASARVLSLREPTTKEHPASVDTMFAFVSRSL

SEQ ID NO:2 Human TRADE $\alpha$   
 SEQ ID NO:6 Mouse Trade

NGEESIEHPHCHUMCGENIEFTSYMHTONIHSLNPLESSTELISN  
 KQSHARLNGHILHES-ILHETPLNLETNSELNENEAALHES

SEQ ID NO:2 Human TRADE $\alpha$   
 SEQ ID NO:6 Mouse Trade

SSATVVGAVPVQEHSENFTAATDLRYNNILVESASTEDALTMREGLDQ  
 GGQIAHHALESAGNVSESTDSPRHGDGTIVWEOTLAIAQRTPLGGW

SEQ ID NO:2 Human TRADE $\alpha$   
 SEQ ID NO:6 Mouse Trade

ESGAVIHPATQSLPEA 417  
 EDRENILNLPFAFPEA 416

Figure 4

105920 36503/50

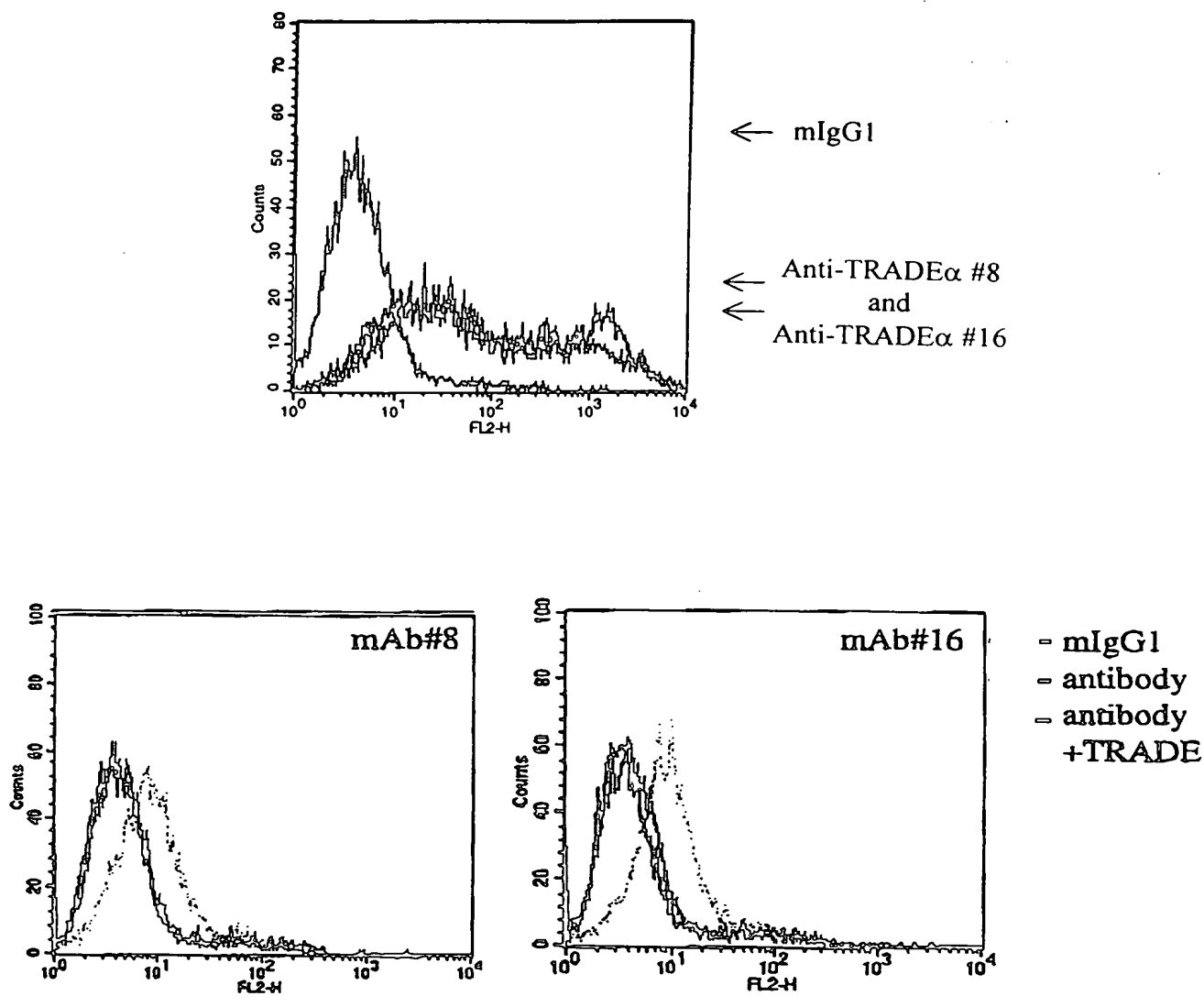


Figure 5

Construct	Relative Luciferase Activity
pcDNA3	~5
TRADEa (0.1ug)	~40
TRADEa (0.5ug)	~110
TRADEa (1ug)	~90
p75NGFR (0.1ug)	~25
p75NGFR (0.5ug)	~85



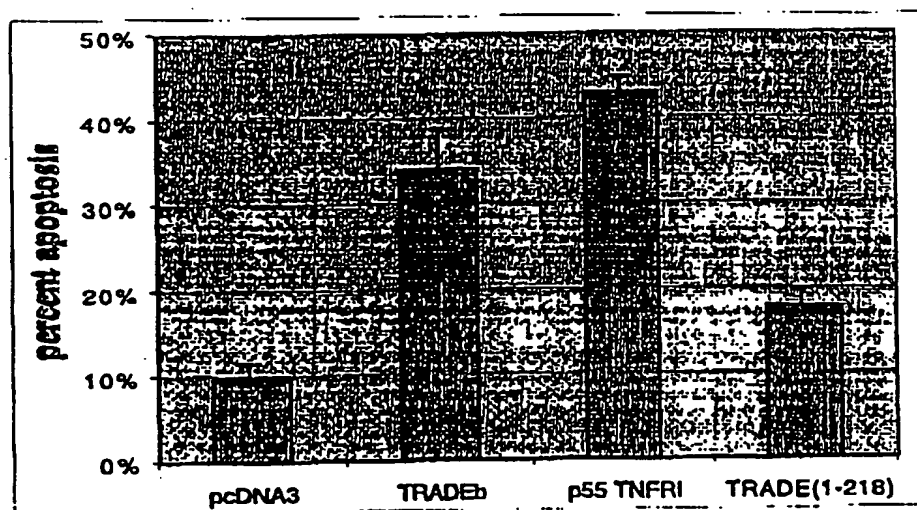
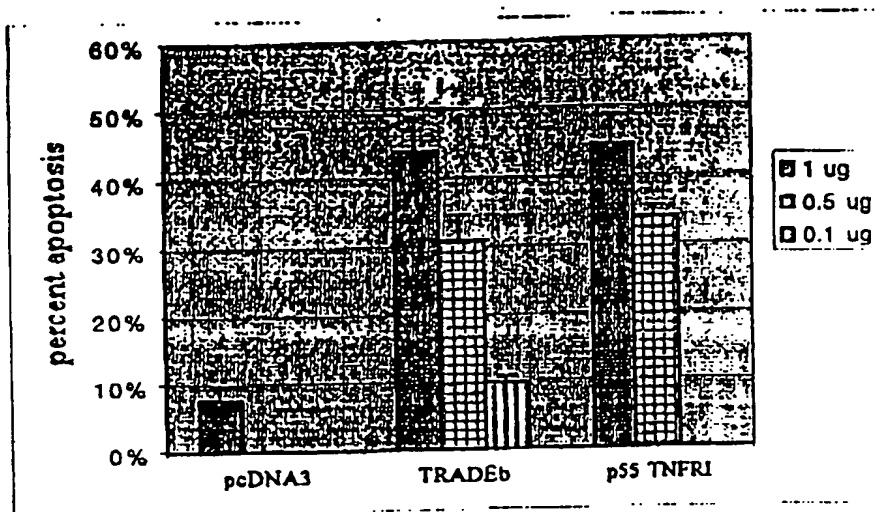


Figure 7

09780530 00000000

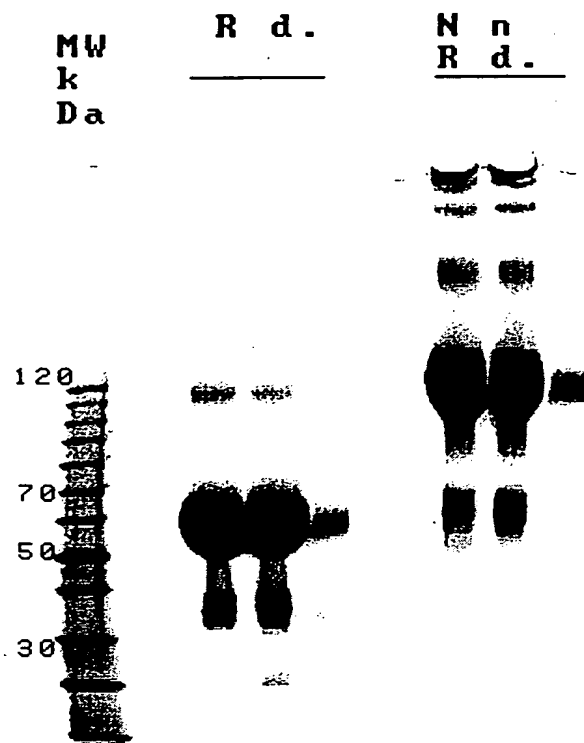
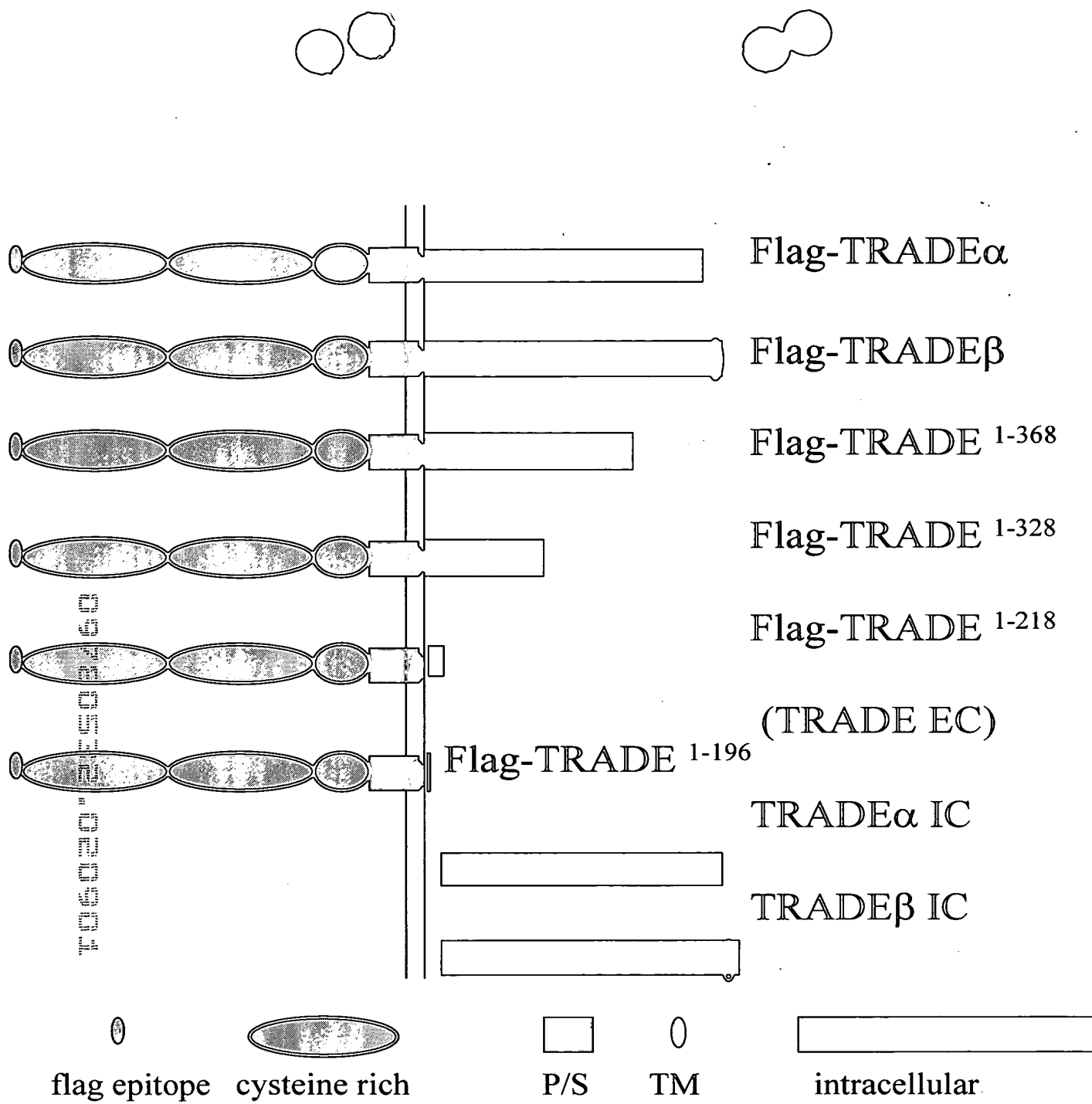


Figure 8



## Deletion analysis

FIGURE 9

105030-2500150

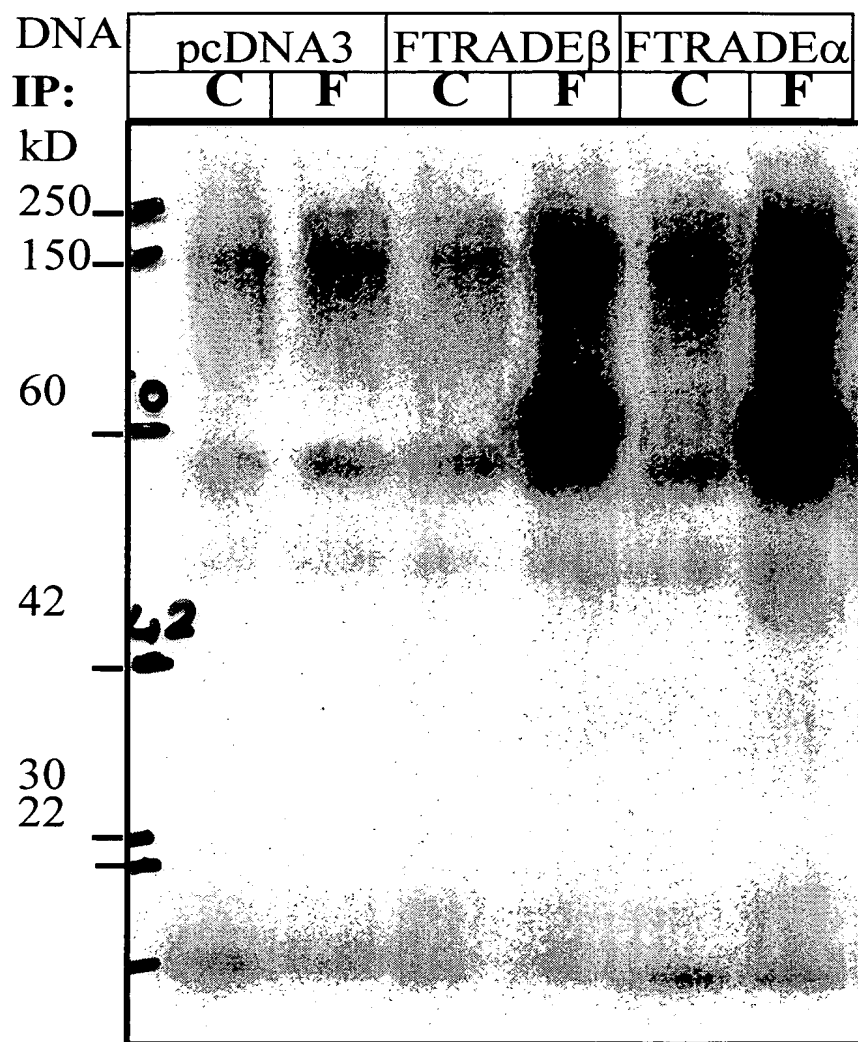
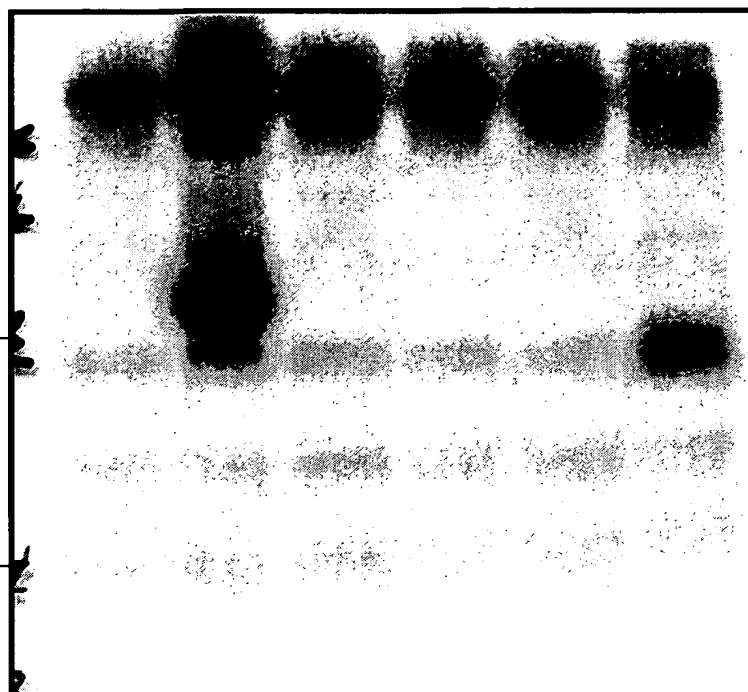


FIGURE 10

A

IP:

F-TRADE $\beta$		F-TRADE <sup>1-328</sup>		F-TRADE <sup>1-368</sup>	
C	F	C	F	C	F

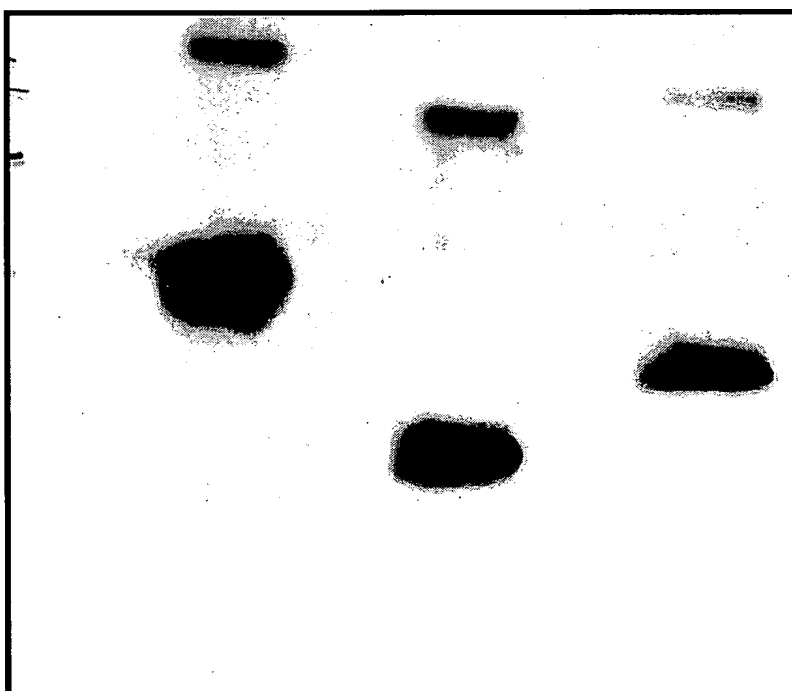


Kinase assay

B

IP:

F-TRADE $\beta$		F-TRADE <sup>1-328</sup>		F-TRADE <sup>1-368</sup>	
C	F	C	F	C	F



anti-Flag blot

FIGURE 11



A

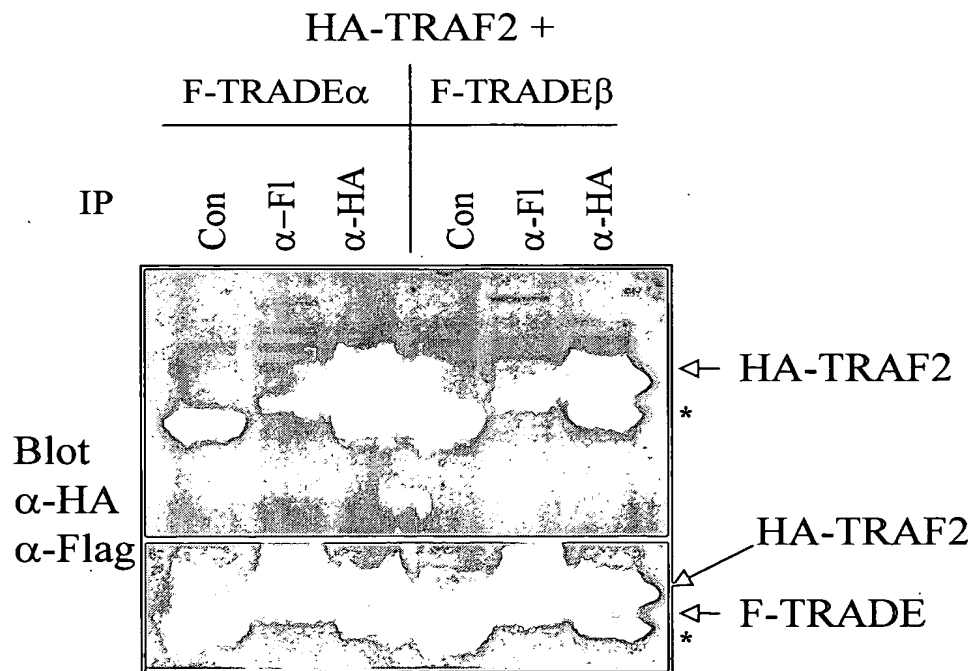
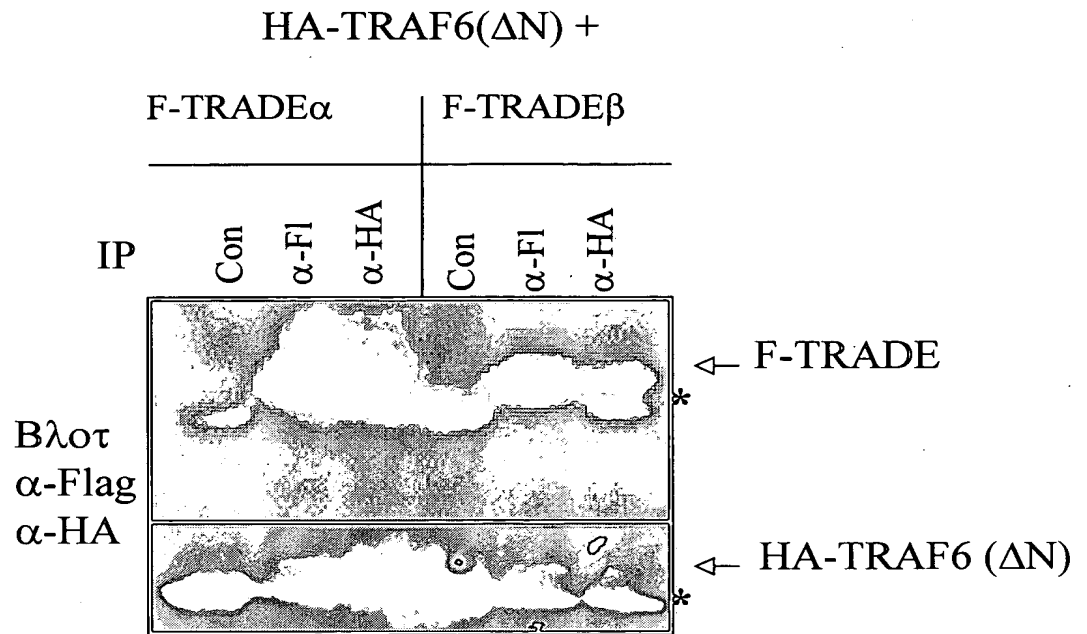


FIGURE 12

09700533.02004  
T06020" 265007650

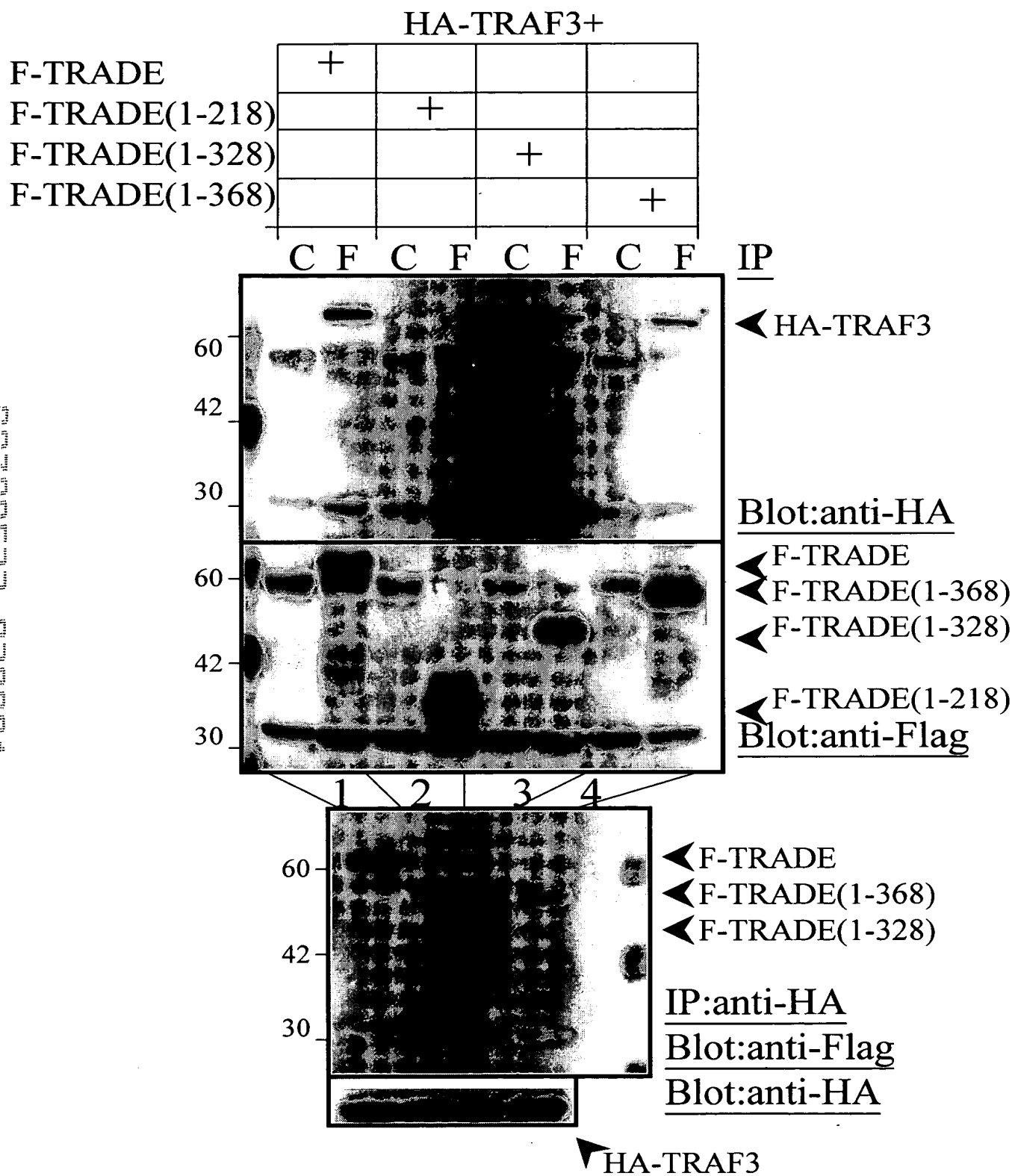


FIGURE 13

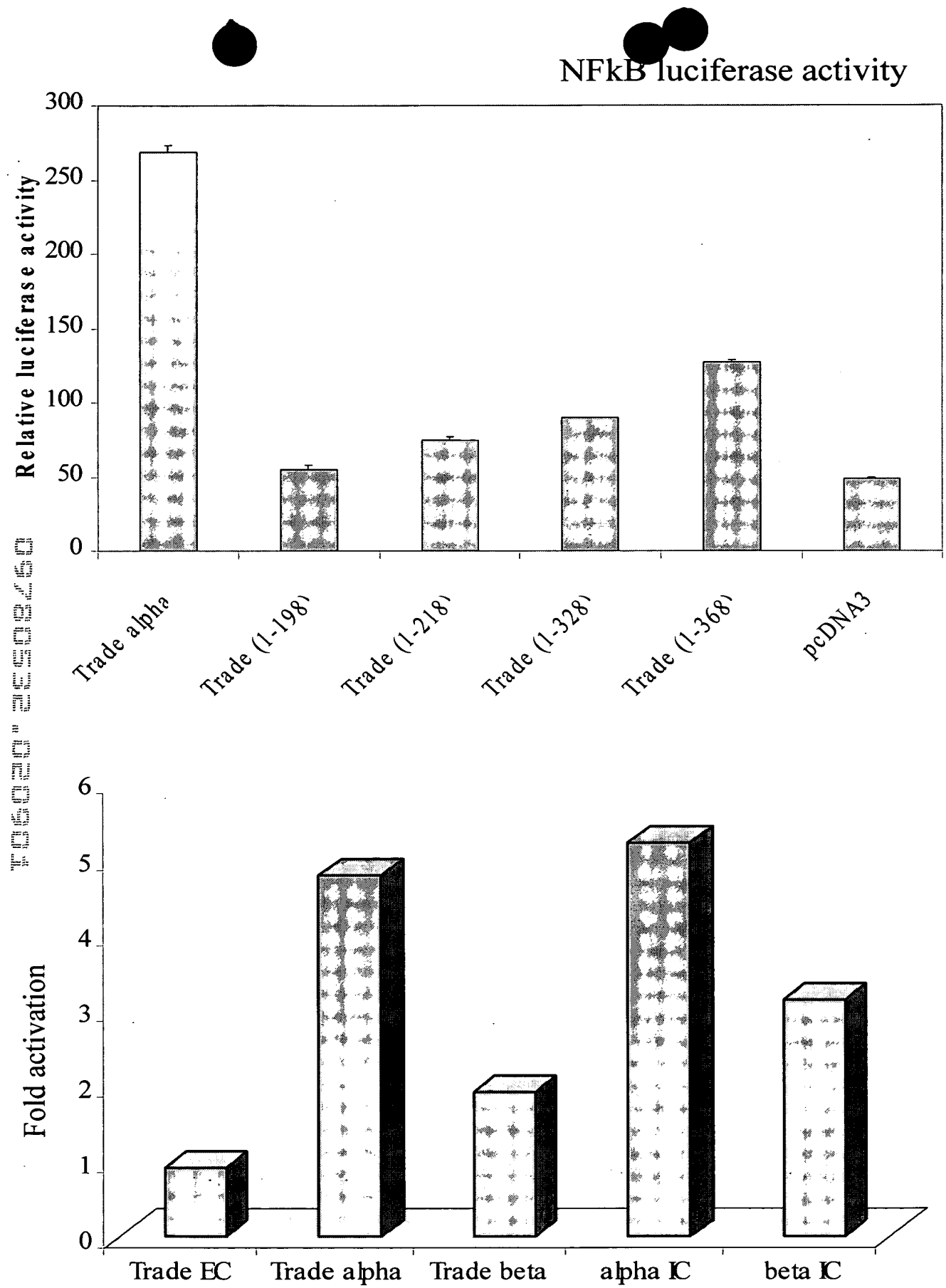


FIGURE 14